SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ozenberger, Brad A.
Jacobsen, J. S. Jonathan Bard
Kajkowski, Eileen Steven Walker

(ii) TITLE OF INVENTION: β-Amyloid Peptide-Binding Proteins and Polynucleotides Encoding the Same

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: American Home Products
(B) STREET: One Campus Drive
(C) CITY: Parsippany
(D) STATE: NJ
(E) COUNTRY: USA
(F) ZIP: 07054

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Walsh, Andrea C.
(B) REGISTRATION NUMBER: 34,988
(C) REFERENCE/DOCKET NUMBER: 98126

(ix) TELECOMMUNICATION INFORMATION:
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(B) TELEFAX: 973-683-4117

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATG CAT ATT TTA AAA GGG TCT CCC AAT GTG ATT CCA CGG GCT CAC GGG        48
Met His Ile Leu Lys Gly Ser Pro Asn Val Ile Pro Arg Ala His Gly
  1               5                  10                  15

CAG AAG AAC ACG CGA AGA GAC GGA ACT GGC CTC TAT CCT ATG CGA GGT        96
Gln Lys Asn Thr Arg Arg Asp Gly Thr Gly Leu Tyr Pro Met Arg Gly
             20                  25                  30

CCC TTT AAG AAC CTC GCC CTG TTG CCC TTC TCC CTC CCG CTC CTG GGC       144
Pro Phe Lys Asn Leu Ala Leu Leu Pro Phe Ser Leu Pro Leu Leu Gly
         35                  40                  45

GGA GGC GGA AGC GGA AGT GGC GAG AAA GTG TCG GTC TCC AAG ATG GCG       192
Gly Gly Gly Ser Gly Ser Gly Glu Lys Val Ser Val Ser Lys Met Ala
     50                  55                  60

GCC GCC TGG CCG TCT GGT CCG TCT GCT CCG GAG GCC GTG ACG GCC AGA       240
Ala Ala Trp Pro Ser Gly Pro Ser Ala Pro Glu Ala Val Thr Ala Arg
 65                  70                  75                  80

CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT ACA GGA CCC TGG GGG       288
Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro Trp Gly
                 85                  90                  95

GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG CTT AAG TGC GAG GAC       336
Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys Glu Asp
            100                 105                 110
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CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA AAA ATA AAT GAC GCT 384
Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn Asp Ala
115 120 125

ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA GCT CAT GTT TCC TGT 432
Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val Ser Cys
130 135 140

TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT TCC AGT GGC AAT GAA ACA 480
Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn Glu Thr
145 150 155 160

CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG CCC ATA TCT TGC CGA 528
His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser Cys Arg
165 170 175

AAT GTA AAT GGC TAT TCC TAC AAA GTG GCA GTC GCA TTG TCT CTT TTT 576
Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser Leu Phe
180 185 190

CTT GGA TGG TTG GGA GCA GAT CGA TTT TAC CTT GGA TAC CCT GCT TTG 624
Leu Gly Trp Leu Gly Ala Asp Arg Phe Tyr Leu Gly Tyr Pro Ala Leu
195 200 205

GGT TTG TTA AAG TTT TGC ACT GTA GGG TTT TGT GGA ATT GGG AGC CTA 672
Gly Leu Leu Lys Phe Cys Thr Val Gly Phe Cys Gly Ile Gly Ser Leu
210 215 220

ATT GAT TTC ATT CTT ATT TCA ATG CAG ATT GTT GGA CCT TCA GAT GGA 720
Ile Asp Phe Ile Leu Ile Ser Met Gln Ile Val Gly Pro Ser Asp Gly
225 230 235 240

AGT AGT TAC ATT ATA GAT TAC TAT GGA ACC AGA CTT ACA AGA CTG AGT 768
Ser Ser Tyr Ile Ile Asp Tyr Tyr Gly Thr Arg Leu Thr Arg Leu Ser
245 250 255

ATT ACT AAT GAA ACA TTT AGA AAA ACG CAA TTA TAT CCA TAA 810
Ile Thr Asn Glu Thr Phe Arg Lys Thr Gln Leu Tyr Pro
260 265

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met His Ile Leu Lys Gly Ser Pro Asn Val Ile Pro Arg Ala His Gly
 1               5                  10                  15

Gln Lys Asn Thr Arg Arg Asp Gly Thr Gly Leu Tyr Pro Met Arg Gly
            20                  25                  30

Pro Phe Lys Asn Leu Ala Leu Leu Pro Phe Ser Leu Pro Leu Leu Gly
        35                  40                  45

Gly Gly Gly Ser Gly Ser Gly Glu Lys Val Ser Val Ser Lys Met Ala
    50                  55                  60

Ala Ala Trp Pro Ser Gly Pro Ser Ala Pro Glu Ala Val Thr Ala Arg
65                  70                  75                  80

Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro Trp Gly
                85                  90                  95

Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys Glu Asp
            100                 105                 110

Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn Asp Ala
        115                 120                 125

Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val Ser Cys
    130                 135                 140

Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn Glu Thr
145                 150                 155                 160

His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser Cys Arg
                165                 170                 175
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Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser Leu Phe
            180                 185                 190

Leu Gly Trp Leu Gly Ala Asp Arg Phe Tyr Leu Gly Tyr Pro Ala Leu
        195                 200                 205

Gly Leu Leu Lys Phe Cys Thr Val Gly Phe Cys Gly Ile Gly Ser Leu
    210                 215                 220

Ile Asp Phe Ile Leu Ile Ser Met Gln Ile Val Gly Pro Ser Asp Gly
225                 230                 235                 240

Ser Ser Tyr Ile Ile Asp Tyr Tyr Gly Thr Arg Leu Thr Arg Leu Ser
                245                 250                 255

Ile Thr Asn Glu Thr Phe Arg Lys Thr Gln Leu Tyr Pro
            260                 265
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